SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Godowski, Paul J. Gurney, Austin L.
- (ii) TITLE OF INVENTION: Tie Ligands
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Dreger, Ginger R.
 - (B) REGISTRATION NUMBER: 33,055
 - (C) REFERENCE/DOCKET NUMBER: P1130
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650/225-3216
 - (B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2290 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- GGCTGAGGGG AGGCCCGGAG CCTTTCTGGG GCCTGGGGGA TCCTCTTGCA 50
 CTGGTGGGTG GAGAGAAGCG CCTGCAGCCA ACCAGGGTCA GGCTGTGCTC 100
- ACAGTTTCCT CTGGCGGCAT GTAAAGGCTC CACAAAGGAG TTGGGAGTTC 150
- AAATGAGGCT GCTGCGGACG GCCTGAGGAT GGACCCCAAG CCCTGGACCT 200
- GCCGAGCGTG GCACTGAGGC AGCGGCTGAC GCTACTGTGA GGGAAAGAAG 250
- GTTGTGAGCA GCCCCGCAGG ACCCCTGGCC AGCCCTGGCC CCAGCCTCTG 300

CCGGAGCCCT	CTGTGGAGGC	AGAGCCAGTG	GAGCCCAGTG	AGGCAGGGCT	350
GCTTGGCAGC	CACCGGCCTG	CAACTCAGGA	ACCCCTCCAG	AGGCCATGGA	400
CAGGCTGCCC	CGCTGACGGC	CAGGGTGAAG	CATGTGAGGA	GCCGCCCCGG	450
AGCCAAGCAG	GAGGGAAGAG	GCTTTCATAG	ATTCTATTCA	CAAAGAATAA	500
CCACCATTTT	GCAAGGACCA	TGAGGCCACT	GTGCGTGACA	TGCTGGTGGC	550
TCGGACTGCT	GGCTGCCATG	GGAGCTGTTG	CAGGCCAGGA	GGACGGTTTT	600
GAGGGCACTG	AGGAGGGCTC	GCCAAGAGAG	TTCATTTACC	TAAACAGGTA	650
CAAGCGGGCG	GGCGAGTCCC	AGGACAAGTG	CACCTACACC	TTCATTGTGC	700
CCCAGCAGCG	GGTCACGGGT	GCCATCTGCG	TCAACTCCAA	GGAGCCTGAG	750
GTGCTTCTGG	AGAACCGAGT	GCATAAGCAG	GAGCTAGAGC	TGCTCAACAA	800
TGAGCTGCTC	AAGCAGAAGC	GGCAGATCGA	GACGCTGCAG	CAGCTGGTGG	850
AGGTGGACGG	CGGCATTGTG	AGCGAGGTGA	AGCTGCTGCG	CAAGGAGAGC	900
CGCAACATGA	ACTCGCGGGT	CACGCAGCTC	TACATGCAGC	TCCTGCACGA	950
GATCATCCGC	AAGCGGGACA	ACGCGTTGGA	GCTCTCCCAG	CTGGAGAACA	1000
GGATCCTGAA	CCAGACAGCC	GACATGCTGC	AGCTGGCCAG	CAAGTACAAG	1050
GACCTGGAGC	ACAAGTACCA	GCACCTGGCC	ACACTGGCCC	ACAACCAATC	1100
AGAGATCATC	GCGCAGCTTG	AGGAGCACTG	CCAGAGGGTG	CCCTCGGCCA	1150
GGCCCGTCCC	CCAGCCACCC	CCCGCTGCCC	CGCCCCGGGT	CTACCAACCA	1200
CCCACCTACA	ACCGCATCAT	CAACCAGATC	TCTACCAACG	AGATCCAGAG	1250
TGACCAGAAC	CTGAAGGTGC	TGCCACCCCC	TCTGCCCACT	ATGCCCACTC	1300
TCACCAGCCT	CCCATCTTCC	ACCGACAAGC	CGTCGGGCCC	ATGGAGAGAC	1350
TGCCTGCAGG	CCCTGGAGGA	TGGCCACGAC	ACCAGCTCCA	TCTACCTGGT	1400
GAAGCCGGAG	AACACCAACC	GCCTCATGCA	GGTGTGGTGC	GACCAGAGAC	1450
ACGACCCCGG	GGGCTGGACC	GTCATCCAGA	GACGCCTGGA	TGGCTCTGTT	1500
AACTTCTTCA	GGAACTGGGA	GACGTACAAG	CAAGGGTTTG	GGAACATTGA	1550
CGGCGAATAC	TGGCTGGGCC	TGGAGAACAT	TTACTGGCTG	ACGAACCAAG	1600
GCAACTACAA	ACTCCTGGTG	ACCATGGAGG	ACTGGTCCGG	CCGCAAAGTC	1650
TTTGCAGAAT	ACGCCAGTTT	CCGCCTGGAA	CCTGAGAGCG	AGTATTATAA	1700
GCTGCGGCTG	GGGCGCTACC	ATGGCAATGC	GGGTGACTCC	TTTACATGGC	1750
ACAACGGCAA	GCAGTTCACC	ACCCTGGACA	GAGATCATGA	TGTCTACACA	1800
GGAAACTGTG	CCCACTACCA	GAAGGGAGGC	TGGTGGTATA	ACGCCTGTGC	1850

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Met
 Arg
 Pro
 Leu
 Cys
 Val
 Thr
 Cys
 Trp
 Leu
 Gly
 Leu
 Leu
 Ala

 Ala
 Met
 Gly
 Ala
 Val
 Ala
 Gly
 Glu
 Glu
 Asp
 Gly
 Phe
 Gly
 Gly
 Phe
 Gly
 Phe
 Gly
 Phe
 Gly
 Gly
 Phe
 Gly
 Phe

Thr Ala Asp Met Leu Gln Leu Ala Ser Lys Tyr Lys Asp Leu Glu

				170					175					180
His	Lys	Tyr	Gln	His 185	Leu	Ala	Thr	Leu	Ala 190	His	Asn	Gln	Ser	Glu 195
Ile	Ile	Ala	Gln	Leu 200	Glu	Glu	His	Cys	Gln 205	Arg	Val	Pro	Ser	Ala 210
Arg	Pro	Val	Pro	Gln 215	Pro	Pro	Pro	Ala	Ala 220	Pro	Pro	Arg	Val	Tyr 225
Gln	Pro	Pro	Thr	Tyr 230	Asn	Arg	Ile	Ile	Asn 235	Gln	Ile	Ser	Thr	Asn 240
Glu	Ile	Gln	Ser	Asp 245	Gln	Asn	Leu	Lys	Val 250	Leu	Pro	Pro	Pro	Leu 255
Pro	Thr	Met	Pro	Thr 260	Leu	Thr	Ser	Leu	Pro 265	Ser	Ser	Thr	Asp	Lys 270
Pro	Ser	Gly	Pro	Trp 275	Arg	Asp	Cys	Leu	Gln 280	Ala	Leu	Glu	Asp	Gly 285
His	Asp	Thr	Ser	Ser 290	Ile	Tyr	Leu	Val	Lys 295	Pro	Glu	Asn	Thr	Asn 300
Arg	Leu	Met	Gln	Val 305	Trp	Cys	Asp	Gln	Arg 310	His	Asp	Pro	Gly	Gly 315
Trp	Thr	Val	Ile	Gln 320	Arg	Arg	Leu	Asp	Gly 325	Ser	Val	Asn	Phe	Phe 330
Arg	Asn	Trp	Glu	Thr 335	Tyr	Lys	Gln	Gly	Phe 340	Gly	Asn	Ile	Asp	Gly 345
Glu	Tyr	Trp	Leu	Gly 350	Leu	Glu	Asn	Ile	Tyr 355	Trp	Leu	Thr	Asn	Gln 360
Gly	Asn	Tyr	Lys	Leu 365	Leu	Val	Thr	Met	Glu 370	Asp	Trp	Ser	Gly	Arg 375
Lys	Val	Phe	Ala	Glu 380	Tyr	Ala	Ser	Phe	Arg 385	Leu	Glu	Pro	Glu	Ser 390
Glu	Tyr	Tyr	Lys	Leu 395	Arg	Leu	Gly	Arg	Tyr 400	His	Gly	Asn	Ala	Gly 405
Asp	Ser	Phe	Thr	Trp 410	His	Asn	Gly	Lys	Gln 415	Phe	Thr	Thr	Leu	Asp 420
Arg	Asp	His	Asp	Val 425	Tyr	Thr	Gly	Asn	Cys 430	Ala	His	Tyr	Gln	Lys 435
Gly	Gly	Trp	Trp	Tyr 440	Asn	Ala	Cys	Ala	His 445	Ser	Asn	Leu	Asn	Gly 450
Val	Trp	Tyr	Arg	Gly 455	Gly	His	Tyr	Arg	Ser 460	Arg	Tyr	Gln	Asp	Gly 465
Val	Tyr	Trp	Ala	Glu 470	Phe	Arg	Gly	Gly	Ser 475	Tyr	Ser	Leu	Lys	Lys 480

Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His 485 493 490

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3355 base pairs
- (B) TYPE: Nucleic Acid(C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCAGCTGGTT	ACTGCATTTC	TCCATGTGGC	AGACAGAGCA	AAGCCACAAC	50
GCTTTCTCTG	CTGGATTAAA	GACGGCCCAC	AGACCAGAAC	TTCCACTATA	100
CTACTTAAAA	TTACATAGGT	GGCTTGTCAA	ATTCAATTGA	TTAGTATTGT	150
AAAAGGAAAA	AGAAGTTCCT	TCTTACAGCT	TGGATTCAAC	GGTCCAAAAC	200
AAAAATGCAG	CTGCCATTAA	AGTCTCAGAT	GAACAAACTT	CTACACTGAT	250
TTTTAAAATC	AAGAATAAGG	GCAGCAAGTT	TCTGGATTCA	CTGAATCAAC	300
AGACACAAAA	AGCTGGCAAT	ATAGCAACTA	TGAAGAGAAA	AGCTACTAAT	350
AAAATTAACC	CAACGCATAG	AAGACTTTTT	TTTCTCTTCT	AAAAACAACT	400
AAGTAAAGAC	ТТАААТТТАА	ACACATCATT	TTACAACCTC	ATTTCAAAAT	450
GAAGACTTTT	ACCTGGACCC	TAGGTGTGCT	ATTCTTCCTA	CTAGTGGACA	500
CTGGACATTG	CAGAGGTGGA	CAATTCAAAA	ТТАААААААТ	AAACCAGAGA	550
AGATACCCTC	GTGCCACAGA	TGGTAAAGAG	GAAGCAAAGA	AATGTGCATA	600
CACATTCCTG	GTACCTGAAC	AAAGAATAAC	AGGGCCAATC	TGTGTCAACA	650
CCAAGGGGCA	AGATGCAAGT	ACCATTAAAG	ACATGATCAC	CAGGATGGAC	700
CTTGAAAACC	TGAAGGATGT	GCTCTCCAGG	CAGAAGCGGG	AGATAGATGT	750
TCTGCAACTG	GTGGTGGATG	TAGATGGAAA	CATTGTGAAT	GAGGTAAAGC	800
TGCTGAGAAA	GGAAAGCCGT	AACATGAACT	CTCGTGTTAC	TCAACTCTAT	850
ATGCAATTAT	TACATGAGAT	TATCCGTAAG	AGGGATAATT	CACTTGAACT	900
TTCCCAACTG	GAAAACAAAA	TCCTCAATGT	CACCACAGAA	ATGTTGAAGA	950
TGGCAACAAG	ATACAGGGAA	CTAGAGGTGA	AATACGCTTC	CTTGACTGAT	1000
CTTGTCAATA	ACCAATCTGT	GATGATCACT	TTGTTGGAAG	AACAGTGCTT	1050
GAGGATATTT	TCCCGACAAG	ACACCCATGT	GTCTCCCCCA	CTTGTCCAGG	1100
TGGTGCCACA	ACATATTCCT	AACAGCCAAC	AGTATACTCC	TGGTCTGCTG	1150
GGAGGTAACG	AGATTCAGAG	GGATCCAGGT	TATCCCAGAG	ATTTAATGCC	1200

ACCACCTGAT CTGGCAACTT CTCCCACCAA AAGCCCTTTC AAGATACCAC 1250 CGGTAACTTT CATCAATGAA GGACCATTCA AAGACTGTCA GCAAGCAAAA 1300 GAAGCTGGGC ATTCGGTCAG TGGGATTTAT ATGATTAAAC CTGAAAACAG 1350 CAATGGACCA ATGCAGTTAT GGTGTGAAAA CAGTTTGGAC CCTGGGGGTT 1400 GGACTGTTAT TCAGAAAAGA ACAGACGGCT CTGTCAACTT CTTCAGAAAT 1450 TGGGAAAATT ATAAGAAAGG GTTTGGAAAC ATTGACGGAG AATACTGGCT 1500 TGGACTGGAA AATATCTATA TGCTTAGCAA TCAAGATAAT TACAAGTTAT 1550 TGATTGAATT AGAAGACTGG AGTGATAAAA AAGTCTATGC AGAATACAGC 1600 AGCTTTCGTC TGGAACCTGA AAGTGAATTC TATAGACTGC GCCTGGGAAC 1650 TTACCAGGGA AATGCAGGGG ATTCTATGAT GTGGCATAAT GGTAAACAAT 1700 TCACCACACT GGACAGAGAT AAAGATATGT ATGCAGGAAA CTGCGCCCAC 1750 TTTCATAAAG GAGGCTGGTG GTACAATGCC TGTGCACATT CTAACCTAAA 1800 TGGAGTATGG TACAGAGGAG GCCATTACAG AAGCAAGCAC CAAGATGGAA 1850 TTTTCTGGGC CGAATACAGA GGCGGGTCAT ACTCCTTAAG AGCAGTTCAG 1900 ATGATGATCA AGCCTATTGA CTGAAGAGAG ACACTCGCCA ATTTAAATGA 1950 CACAGAACTT TGTACTTTTC AGCTCTTAAA AATGTAAATG TTACATGTAT 2000 ATTACTTGGC ACAATTTATT TCTACACAGA AAGTTTTTAA AATGAATTTT 2050 ACCGTAACTA TAAAAGGGAA CCTATAAATG TAGTTTCATC TGTCGTCAAT 2100 TACTGCAGAA AATTATGTGT ATCCACAACC TAGTTATTTT AAAAATTATG 2150 TTGACTAAAT ACAAAGTTTG TTTTCTAAAA TGTAAATATT TGCCACAATG 2200 TAAAGCAAAT CTTAGCTATA TTTTAAATCA TAAATAACAT GTTCAAGATA 2250 CTTAACAATT TATTTAAAAT CTAAGATTGC TCTAACGTCT AGTGAAAAAA 2300 GACAGAAAAT TAGGGAGAAA CTTCTAGTTT TGCCAATAGA AAATGTTCTT 2400 CCATTGAATA AAAGTTATTT CAAATTGAAT TTGTGCCTTT CACACGTAAT 2450 GATTAAATCT GAATTCTTAA TAATATATCC TATGCTGATT TTCCCAAAAC 2500 ATGACCCATA GTATTAAATA CATATCATTT TTAAAAATAA AAAAAAACCC 2550 AAAAATAATG CATGCATAAT TTAAATGGTC AATTTATAAA GACAAATCTA 2600 TGAATGAATT TTTCAGTGTT ATCTTCATAT GATATGCTGA ACACCAAAAT 2650 CTCCAGAAAT GCATTTTATG TAGTTCTAAA ATCAGCAAAA TATTGGTATT 2700 ACAAAAATGC AGAATATTTA GTGTGCTACA GATCTGAATT ATAGTTCTAA 2750

TTTATTATTA CTTTTTTCT AATTTACTGA TCTTACTACT ACAAAGAAAA 2800 AAAAACCCAA CCCATCTGCA ATTCAAATCA GAAAGTTTGG ACAGCTTTAC 2850 AAGTATTAGT GCATGCTCAG AACAGGTGGG ACTAAAACAA ACTCAAGGAA 2900 CTGTTGGCTG TTTTCCCGAT ACTGAGAATT CAACAGCTCC AGAGCAGAAG 2950 CCACAGGGGC ATAGCTTAGT CCAAACTGCT AATTTCATTT TACAGTGTAT 3000 GTAACGCTTA GTCTCACAGT GTCTTTAACT CATCTTTGCA ATCAACAACT 3050 TTACTAGTGA CTTTCTGGAA CAATTTCCTT TCAGGAATAC ATATTCACTG 3100 CTTAGAGGTG ACCTTGCCTT AATATATTTG TGAAGTTAAA ATTTTAAAGA 3150 TAGCTCATGA AACTTTTGCT TAAGCAAAAA GAAAACCTCG AATTGAAATG 3200 TGTGAGGCAA ACTATGCATG GGAATAGCTT AATGTGAAGA TAATCATTTG 3250 GACAACTCAA ATCCATCAAC ATGACCAATG TTTTTCATCT GCCACATCTC 3300 AAAATAAAC TTCTGGTGAA ACAAATTAAA CAAAATATCC AAACCTCAAA 3350 AAAAA 3355

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 491 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Thr Phe Thr Trp Thr Leu Gly Val Leu Phe Phe Leu Leu Val Asp Thr Gly His Cys Arg Gly Gly Gln Phe Lys Ile Lys Lys Ile Asn Gln Arg Arg Tyr Pro Arg Ala Thr Asp Gly Lys Glu Glu Ala Lys Lys Cys Ala Tyr Thr Phe Leu Val Pro Glu Gln Arg Ile Thr Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr Ile Lys Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp Val Leu Ser Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val 100 Val Asp Val Asp Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg 110 115 Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met 125

130

135

Gln	Leu	Leu	His	Glu 140	Ile	Ile	Arg	Lys	Arg 145	Asp	Asn	Ser	Leu	Glu 150
Leu	Ser	Gln	Leu	Glu 155	Asn	Lys	Ile	Leu	Asn 160	Val	Thr	Thr	Glu	Met 165
Leu	Lys	Met	Ala	Thr 170	Arg	Tyr	Arg	Glu	Leu 175	Glu	Val	Lys	Tyr	Ala 180
Ser	Leu	Thr	Asp	Leu 185	Val	Asn	Asn	Gln	Ser 190	Val	Met	Ile	Thr	Leu 195
Leu	Glu	Glu	Gln	Cys 200	Leu	Arg	Ile	Phe	Ser 205	Arg	Gln	Asp	Thr	His 210
Val	Ser	Pro	Pro	Leu 215	Val	Gln	Val	Val	Pro 220	Gln	His	Ile	Pro	Asn 225
Ser	Gln	Gln	Tyr	Thr 230	Pro	Gly	Leu	Leu	Gly 235	Gly	Asn	Glu	Ile	Gln 240
Arg	Asp	Pro	Gly	Tyr 245	Pro	Arg	Asp	Leu	Met 250	Pro	Pro	Pro	Asp	Leu 255
Ala	Thr	Ser	Pro	Thr 260	Lys	Ser	Pro	Phe	Lys 265	Ile	Pro	Pro	Val	Thr 270
Phe	Ile	Asn	Glu	Gly 275	Pro	Phe	Lys	Asp	Cys 280	Gln	Gln	Ala	Lys	Glu 285
Ala	Gly	His	Ser	Val 290	Ser	Gly	Ile	Tyr	Met 295	Ile	Lys	Pro	Glu	Asn 300
Ser	Asn	Gly	Pro	Met 305	Gln	Leu	Trp	Cys	Glu 310	Asn	Ser	Leu	Asp	Pro 315
Gly	Gly	Trp	Thr	Val 320	Ile	Gln	Lys	Arg	Thr 325	Asp	Gly	Ser	Val	Asn 330
Phe	Phe	Arg	Asn	Trp 335	Glu	Asn	Tyr	Lys	Lys 340	Gly	Phe	Gly	Asn	Ile 345
Asp	Gly	Glu	Tyr	Trp 350	Leu	Gly	Leu	Glu	Asn 355	Ile	Tyr	Met	Leu	Ser 360
Asn	Gln	Asp	Asn	Tyr 365	Lys	Leu	Leu	Ile	Glu 370	Leu	Glu	Asp	Trp	Ser 375
Asp	Lys	Lys	.Val	Tyr 380	Ala	Glu	Tyr	Ser	Ser 385	Phe	Arg	Leu	Glu	Pro 390
Glu	Ser	Glu	Phe	Tyr 395	Arg	Leu	Arg	Leu	Gly 400	Thr	Tyr	Gln	Gly	Asn 405
Ala	Gly	Asp	Ser	Met 410	Met	Trp	His	Asn	Gly 415	Lys	Gln	Phe	Thr	Thr 420
Leu	Asp	Arg	Asp	Lys 425	Asp	Met	Tyr	Ala	Gly 430	Asn	Cys	Ala	His	Phe 435
His	Lys	Gly	Gly	Trp	Trp	Tyr	Asn	Ala	Cys	Ala	His	Ser	Asn	Leu

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Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys His Gln 455

Asp Gly Ile Phe Trp Ala Gly Tyr Arg Gly Gly Sor Tyr Ser Ley

Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly Ser Tyr Ser Leu 470 475 480

Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp 485 490 491

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1780 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCTCAGAGG	CCCCACTGGA	CCCTCGGCTC	TTCCTTGGAC	TTCTTGTGTG	50
TTCTGTGAGC	TTCGCTGGAT	TCAGGGTCTT	GGGCATCAGA	GGTGAGAGGG	100
TGGGAAGGTC	CGCCGCGATG	GGGAAGCCCT	GGCTGCGTGC	GCTACAGCTG	150
CTGCTCCTGC	TGGGCGCGTC	GTGGGCGCGG	GCGGGCGCCC	CGCGCTGCAC	200
CTACACCTTC	GTGCTGCCCC	CGCAGAAGTT	CACGGGCGCT	GTGTGCTGGA	250
GCGGCCCCGC	ATCCACGCGG	GCGACGCCCG	AGGCCGCCAA	CGCCAGCGAG	300
CTGGCGGCGC	TGCGCATGCG	CGTCGGCCGC	CACGAGGAGC	TGTTACGCGA	350
GCTGCAGAGG	CTGGCGGCGG	CCGACGGCGC	CGTGGCCGGC	GAGGTGCGCG	400
CGCTGCGCAA	GGAGAGCCGC	GGCCTGAGCG	CGCGCCTGGG	CCAGTTGCGC	450
GCGCAGCTGC	AGCACGAGGC	GGGCCCGGG	GCGGGCCCGG	GGGCGGATCT	500
GGGGGCGGAG	CCTGCCGCGG	CGCTGGCGCT	GCTCGGGGAG	CGCGTGCTCA	550
ACGCGTCCGC	CGAGGCTCAG	CGCGCAGCCG	CCCGGTTCCA	CCAGCTGGAC	600
GTCAAGTTCC	GCGAGCTGGC	GCAGCTCGTC	ACCCAGCAGA	GCAGTCTCAT	650
CGCCCGCCTG	GAGCGCCTGT	GCCCGGGAGG	cgcgggcggg	CAGCAGCAGG	700
TCCTGCCGCC	ACCCCCACTG	GTGCCTGTGG	TTCCGGTCCG	TCTTGTGGGT	750
AGCACCAGTG	ACACCAGTAG	GATGCTGGAC	CCAGCCCCAG	AGCCCCAGAG	800
AGACCAGACC	CAGAGACAGC	AGGAGCCCAT	GGCTTCTCCC	ATGCCTGCAG	850
GTCACCCTGC	GGTCCCCACC	AAGCCTGTGG	GCCCGTGGCA	GGATTGTGCA	900
GAGGCCCGCC	AGGCAGGCCA	TGAACAGAGT	GGAGTGTATG	AACTGCGAGT	950
GGGCCGTCAC	GTAGTGTCAĢ	TATGGTGTGA	GCAGCAACTG	GAGGGTGGAG	1000

GCTGGACTGT GATCCAGCGG AGGCAAGATG GTTCAGTCAA CTTCTTCACT 1050 ACCTGGCAGC ACTATAAGGC GGGCTTTGGG CGGCCAGACG GAGAATACTG 1100 GCTGGGCCTT GAACCCGTGT ATCAGCTGAC CAGCCGTGGG GACCATGAGC 1150 TGCTGGTTCT CCTGGAGGAC TGGGGGGGCC GTGGAGCACG TGCCCACTAT 1200 GATGGCTTCT CCCTGGAACC CGAGAGCGAC CACTACCGCC TGCGGCTTGG 1250 CCAGTACCAT GGTGATGCTG GAGACTCTCT TTCCTGGCAC AATGACAAGC 1300 CCTTCAGCAC CGTGGATAGG GACCGAGACT CCTATTCTGG TAACTGTGCC 1350 CTGTACCAGC GGGGAGGCTG GTGGTACCAT GCCTGTGCCC ACTCCAACCT 1400 CAACGGTGTG TGGCACCACG GCGGCCACTA CCGAAGCCGC TACCAGGATG 1450 GTGTCTACTG GGCTGAGTTT CGTGGTGGGG CATATTCTCT CAGGAAGGCC 1500 GCCATGCTCA TTCGGCCCCT GAAGCTGTGA CTCTGTGTTC CTCTGTCCCC 1550 TAGGCCCTAG AGGACATTGG TCAGCAGGAG CCCAAGTTGT TCTGGCCACA 1600 CCTTCTTTGT GGCTCAGTGC CAATGTGTCC CACAGAACTT CCCACTGTGG 1650 ATCTGTGACC CTGGGCGCTG AAAATGGGAC CCAGGAATCC CCCCGTCAA 1700 TATCTTGGCC TCAGATGGCT CCCCAAGGTC ATTCATATCT CGGTTTGAGC 1750 TCATATCTTA TAATAACACA AAGTAGCCAC 1780

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Lys Pro Trp Leu Arg Ala Leu Gln Leu Leu Leu Leu 1 5 10 15

Gly Ala Ser Trp Ala Arg Ala Gly Ala Pro Arg Cys Thr Tyr Thr 20 25 30

Phe Val Leu Pro Pro Gln Lys Phe Thr Gly Ala Val Cys Trp Ser 35 40 45

Gly Pro Ala Ser Thr Arg Ala Thr Pro Glu Ala Ala Asn Ala Ser
50 55 60

Glu Leu Ala Ala Leu Arg Met Arg Val Gly Arg His Glu Glu Leu 65 70 75

Leu Arg Glu Leu Gln Arg Leu Ala Ala Ala Asp Gly Ala Val Ala 80 85 90

Gly Glu Val Arg Ala Leu Arg Lys Glu Ser Arg Gly Leu Ser Ala 95 100 105

Arg	Leu	Gly	Gln	Leu 110	Arg	Ala	Gln	Leu	Gln 115	His	Glu	Ala	Gly	Pro 120
Gly	Ala	Gly	Pro	Gly 125	Ala	Asp	Leu	Gly	Ala 130	Glu	Pro	Ala	Ala	Ala 135
Leu	Ala	Leu	Leu	Gly 140	Glu	Arg	Val	Leu	Asn 145	Ala	Ser	Ala	Glu	Ala 150
Gln	Arg	Ala	Ala	Ala 155	Arg	Phe	His	Gln	Leu 160	Asp	Val	Lys	Phe	Arg 165
Glu	Leu	Ala	Gln	Leu 170	Val	Thr	Gln	Gln	Ser 175	Ser	Leu	Ile	Ala	Arg 180
Leu	Glu	Arg	Leu	Cys 185	Pro	Gly	Gly	Ala	Gly 190	Gly	Gln	Gln	Gln	Val 195
Leu	Pro	Pro	Pro	Pro 200	Leu	Val	Pro	Val	Val 205	Pro	Val	Arg	Leu	Val 210
Gly	Ser	Thr	Ser	Asp 215	Thr	Ser	Arg	Met	Leu 220	Asp	Pro	Ala	Pro	Glu 225
Pro	Gln	Arg	Asp	Gln 230	Thr	Gln	Arg	Gln	Gln 235	Glu	Pro	Met	Ala	Ser 240
Pro	Met	Pro	Ala	Gly 245	His	Pro	Ala	Val	Pro 250	Thr	Lys	Pro	Val	Gly 255
Pro	Trp	Gln	Asp	Cys 260	Ala	Glu	Ala	Arg	Gln 265	Ala	Gly	His	Glu	Gln 270
Ser	Gly	Val	Tyr	Glu 275	Leu	Arg	Val	Gly	Arg 280	His	Val	Val	Ser	Val 285
Trp	Cys	Glu	Gln	Gln 290	Leu	Glu	Gly	Gly	Gly 295	Trp	Thr	Val	Ile	Gln 300
Arg	Arg	Gln	Asp	Gly 305	Ser	Val	Asn	Phe	Phe 310	Thr	Thr	Trp	Gln	His 315
Tyr	Lys	Ala	Gly	Phe 320	Gly	Arg	Pro	Asp	Gly 325	Glu	Tyr	Trp	Leu	Gly 330
Leu	Glu	Pro	Val	Tyr 335	Gln	Leu	Thr	Ser	Arg 340	Gly	Asp	His	Glu	Leu 345
Leu	Val	Leu	Leu	Glu 350	Asp	Trp	Gly	Gly	Arg 355	Gly	Ala	Arg	Ala	His 360
Tyr	Asp	Gly	Phe	Ser 365	Leu	Glu	Pro	Glu	Ser 370	Asp	His	Tyr	Arg	Leu 375
Arg	Leu	Gly	Gln	Tyr 380	His	Gly	Asp	Ala	Gly 385	Asp	Ser	Leu	Ser	Trp 390
His	Asn	Asp	Lys	Pro 395	Phe	Ser	Thr	Val	Asp 400	Arg	Asp	Arg	Asp	Ser 405
Tyr	Ser	Gly	Asn	Cys	Ala	Leu	Tyr	Gln	Arg	Gly	Gly	Trp	Trp	Tyr

His Ala Cys Ala His Ser Asn Leu Asn Gly Val Trp His His Gly 435

Gly His Tyr Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu 440

Phe Arg Gly Gly Ala Tyr Ser Leu Arg Lys Ala Ala Met Leu Ile 465

Arg Pro Leu Lys Leu

470

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
- GCTGACGAAC CAAGGCAACT ACAAACTCCT GGT 33
- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: Nucleic Acid
 - (b) TIPE. Nucleic Acto
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCGGCCGGA CCAGTCCTCC ATGGTCACCA GGAGTTTGTA G 41

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGTGGTGAAC TGCTTGCCGT TGTGCCATGT AAA 33

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGGTTATCC CAGAGATTTA ATGCCACCA 29

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTGGTGGGAG AAGTTGCCAG ATCAGGTGGT GGCA 34

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCACACCAT AACTGCATTG GTCCA 25

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGTAGTTCC AGTATGGTGT GAGCAGCAAC TGGA 34

- (2) INFORMATION FOR SEQ ID NO:14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGTCCAGCCT CCACCCTCCA GTTGCT 26

- (2) INFORMATION FOR SEQ ID NO:15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCAGTCCT CCAGGAGAAC CAGCA 25

- (2) INFORMATION FOR SEQ ID NO:16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2042 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGGACGCGT	GGGTGAAATT	GAAAATCAAG	ATAAAAATGT	TCACAATTAA	50
GCTCCTTCTT	TTTATTGTTC	CTCTAGTTAT	TTCCTCCAGA	ATTGATCAAG	100
ACAATTCATC	ATTTGATTCT	CTATCTCCAG	AGCCAAAATC	AAGATTTGCT	150
ATGTTAGACG	ATGTAAAAAT	TTTAGCCAAT	GGCCTCCTTC	AGTTGGGACA	200
TGGTCTTAAA	GACTTTGTCC	ATAAGACGAA	GGGCCAAATT	AATGACATAT	250
TTCAAAAACT	CAACATATTT	GATCAGTCTT	TTTATGATCT	ATCGCTGCAA	300
ACCAGTGAAA	TCAAAGAAGA	AGAAAAGGAA	CTGAGAAGAA	СТАСАТАТАА	350
ACTACAAGTC	AAAAATGAAG	AGGTAAAGAA	TATGTCACTT	GAACTCAACT	400
CAAAACTTGA	AAGCCTCCTA	GAAGAAAAA	TTCTACTTCA	ACAAAAAGTG	450
AAATATTTAG	AAGAGCAACT	AACTAACTTA	ATTCAAAATC	AACCTGAAAC	500
TCCAGAACAC	CCAGAAGTAA	CTTCACTTAA	AACTTTTGTA	GAAAAACAAG	550
ATAATAGCAT	CAAAGACCTT	CTCCAGACCG	TGGAAGACCA	ATATAAACAA	600
TTAAACCAAC	AGCATAGTCA	AATAAAAGAA	ATAGAAAATC	AGCTCAGAAG	650
GACTAGTATT	CAAGAACCCA	CAGAAATTTC	TCTATCTTCC	AAGCCAAGAG	700
CACCAAGAAC	TACTCCCTTT	CTTCAGTTGA	ATGAAATAAG	AAATGTAAAA	750
CATGATGGCA	TTCCTGCTGA	ATGTACCACC	ATTTATAACA	GAGGTGAACA	800
TACAAGTGGC	ATGTATGCCA	TCAGACCCAG	CAACTCTCAA	GTTTTTCATG	850
TCTACTGTGA	TGTTATATCA	GGTAGTCCAT	GGACATTAAT	TCAACATCGA	900
ATAGATGGAT	CACAAAACTT	CAATGAAACG	TGGGAGAACT	ACAAATATGG	950
TTTTGGGAGG	CTTGATGGAG	AATTTTGGTT	GGGCCTAGAG	AAGATATACT	1000
CCATAGTGAA	GCAATCTAAT	TATGTTTTAC	GAATTGAGTT	GGAAGACTGG	1050

AAAGACAACA AACATTATAT TGAATATTCT TTTTACTTGG GAAATCACGA 1100 AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCCAATG 1150 CAATCCCGGA AAACAAAGAT TTGGTGTTTT CTACTTGGGA TCACAAAGCA 1200 AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250 TGATGAGTGT GGAGAAAACA ACCTAAATGG TAAATATAAC AAACCAAGAG 1300 CAAAATCTAA GCCAGAGAGG AGAAGAGGAT TATCTTGGAA GTCTCAAAAT 1350 GGAAGGTTAT ACTCTATAAA ATCAACCAAA ATGTTGATCC ATCCAACAGA 1400 TTCAGAAAGC TTTGAATGAA CTGAGGCAAT TTAAAGGCAT ATTTAACCAT 1450 TAACTCATTC CAAGTTAATG TGGTCTAATA ATCTGGTATA AATCCTTAAG 1500 AGAAAGCTTG AGAAATAGAT TTTTTTTATC TTAAAGTCAC TGTCTATTTA 1550 AGATTAAACA TACAATCACA TAACCTTAAA GAATACCGTT TACATTTCTC 1600 AATCAAAATT CTTATAATAC TATTTGTTTT AAATTTTGTG ATGTGGGAAT 1650 CAATTTTAGA TGGTCACAAT CTAGATTATA ATCAATAGGT GAACTTATTA 1700 AATAACTTTT CTAAATAAAA AATTTAGAGA CTTTTATTTT AAAAGGCATC 1750 ATATGAGCTA ATATCACAAC TTTCCCAGTT TAAAAAACTA GTACTCTTGT 1800 TAAAACTCTA AACTTGACTA AATACAGAGG ACTGGTAATT GTACAGTTCT 1850 TAAATGTTGT AGTATTAATT TCAAAACTAA AAATCGTCAG CACAGAGTAT 1900 GTGTAAAAAT CTGTAATACA AATTTTTAAA CTGATGCTTC ATTTTGCTAC 1950 AAGCAGAATT AAATACTGTA TTAAAATAAG TTCGCTGTCT TT 2042

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 460 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Phe Thr Ile Lys Leu Leu Phe Ile Val Pro Leu Val Ile 1 5 10 15

Ser Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser 20 25 30

Pro Glu Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile

Leu Ala Asn Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe
50 55 60

Val His Lys Thr Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu Lys Glu Leu Arg Arg Thr Thr Tyr Lys 95 100 Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met Ser Leu Glu Leu 115 Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile Leu Leu Gln 125 130 Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu Lys 155 160 Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln 175 . Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln 185 190 195 Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu 205 Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr 220 Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His 250 Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe 265 His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile 285 Gln His Arg Tle Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu 295 Asn Tyr Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu 305 310 Gly Leu Glu Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val 320 325 Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile 340 345 335 Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr Asn Tyr Thr Leu 350 355 360 His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala Ile Pro Glu

365 370 375 Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp His 395 Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro 410 415 Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys 425 430 Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu 440 Ile His Pro Thr Asp Ser Glu Ser Phe Glu 455